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Joint Regression Analysis applied to genotype stability evaluation over years

Zastosowanie analizy regresji łącznej do badania stabilności genotypów w doświadczeniach wieloletnich

Most genotype differences connected with yield stability are due to genotype × environment interaction. The presence and dimension of this interaction are the factors that determine the performance of genotypes in distinct environments. The environmental factors, like annual rainfall, temperature, diseases or soil fertility, can only explain part of this interaction. Many statistical tools have been developed with the aim to explain the information contained in the GE interaction data matrix. In our work we use the Joint Regression Analysis (JRA), the Zig-Zag Algorithm to estimate the regression coefficients and the multiple comparison tests of Scheffé, Tukey and Bonferroni. We point out not just the limitations of the JRA when used year by year, but also genotype selection advantage from general JRA over years. Data of the Portuguese Plant Breeding Board were used to carry the year and over years analyses of yielding stability of 22 different genotypes of oat (*Avena sativa* L.) at six different locations in the years 2002, 2003 and 2004.

Key words: genotype stability, joint regression analysis, oat

Interakcja genotypowo-środowiskowa jest jednym z głównych źródeł różnic w plonowaniu odmian. Istnienie i zakres interakcji determinuje przydatność odmian w różnych środowiskach. Częściowo możemy ją wyjaśnić poprzez niektóre cechy charakteryzujące środowisko takie jak np.: roczna wielkość opadów, temperatura powietrza, częstość występowania chorób, żyzność gleby. W celu wyjaśnienia interakcji genotypowo-środowiskowej wykorzystujemy w pracy informację zawartą w dwuwymiarowej tabeli danych, stosując przy tym następujące metody statystyczne: analiza regresji łącznej, algorytm naprzemienny Zig-Zag, estymacja parametrów równań regresji oraz testy jednoczesne Scheffego, Tukeya i Bonferroniego. Ponadto dyskutujemy użyteczność metody regresji łącznej do selekcji odmian w doświadczeniach pojedynczych oraz w doświadczeniach wielokrotnych i wieloletnich. Rozważania teoretyczne ilustrujemy danymi pochodzącymi z Portugalskiej Sekcji Hodowli Roślin. Dane dotyczą badania stabilności plonu 22 genotypów owsa (*Avena sativa* L.) na podstawie doświadczeń przeprowadzonych w sześciu miejscowościach w latach 2002, 2003 i 2004.

Słowa kluczowe: analiza regresji łącznej, owies, stabilność genotypów

1. INTRODUCTION

To perform successfully, a certain genotype should be dominant or at least not dominated in consecutive years of evaluation. Then, the stability of parameters is a very important issue in plant breeding programs, and methods for testing and interpreting the genotype × environment interaction have been a matter of concern not only in agronomic literature, but also from the point of view of statistical tools development. Joint regression analysis (JRA) is a powerful tool to analyse this interaction, as was shown for example by Aastveit, and Mejza (1992).

The yield data, obtained for 22 different genotypes of oat (*Avena sativa L.)* at six locations in the years 2002, 2003 and 2004 kindly provided by the Portuguese Plant Breeding Board, were used:
— to study and evaluate genotype stability in three consecutive years, year by year;
— to compare the results over years and to draw conclusions on genotype selection.

We used the JRA year by year and over years. The Zig-Zag Algorithm was be used to estimate the regression coefficients. Multiple comparison tests of Scheffé, Tuckey and Bonferroni were also done.

2. REGRESSION ADJUSTMENT AND UPPER CONTOUR

In the JRA, the environmental index is a synthetic variable used to measure the productive capacity of each block by year combination.

Since in our problem every genotype is present in each block, this is the complete case. For this case the corresponding environmental indexes are estimated through their average yields, as it can be see in Gusmão (1985 a, b). The next step is to adjust linear regressions, one per genotype, of yields on environmental indexes.

Considering J genotypes occurring in each of the b blocks, where b is the number of locations multiplied by the number of replications, $y_{i,j}$ as the yield for the jth genotype on the ith block, $j = 1,…,J$; $i = 1,…,b$, then to adjust the regression coefficients we minimize the objective function

$$S(\boldsymbol{\alpha}^J, \boldsymbol{\beta}^J, \boldsymbol{x}^b) = \sum_{j=1}^{J} \sum_{i=1}^{b} p_{i,j} (y_{i,j} - \alpha_j - \beta_j x_i)^2$$

The pairs $(\alpha_j, \beta_j, j = 1,…,J$, represent the regression coefficients for the J genotypes, $\boldsymbol{x}^b = (x_1,…,x_b)$ is the vector of environmental indexes, $\boldsymbol{\alpha}^J = (\alpha_1,…,\alpha_J)$ and $\boldsymbol{\beta}^J = (\beta_1,…,\beta_J)$. In the general case $p_{i,j}$, $I = 1,…,b$; $j = 1,…,J$, represent the genotype weight in the block. We will assume $p_{i,j}, = 1$ since we are in the complete case — all genotypes are present in all blocks. The minimization procedure is carried out using the Zig-Zag Algorithm, (see Pereira and Mexia, 2002).

After the adjustment procedure we need to carry on joint representation of regression lines and make the interpretation of upper contour.

The upper contour of the adjusted regression lines on genotypes selection and comparison was introduced by Mexia *et. al*. (1997), and it is shown to be a convex polygonal.

The upper contour is constituted by segments of the adjusted regression lines where each of them corresponds to a range of variation of the environmental indexes in which the corresponding genotype has maximum adjusted yield.

The genotypes whose regressions partake in the upper contour are the dominant ones. The other genotypes must be compared with the dominant ones to check if they are significantly dominated throughout the entire range of environmental indexes.

3. GENOTYPE STABILITY EVALUATION IN PLANT BREEDING: APPLICATION TO OATS BREEDING PROGRAM

Our research is based on the joint regression analysis and multiple comparison methods, on the study of oats yield data. These data were obtained in the experiments carried out in the years 2002, 2003 and 2004 by the Portuguese National Plant Breeding Board, who kindly allowed us to use them. During this period, 22 genotypes were compared at six different locations, as we explain in Table 1.

Table 2 presents the names of genotypes investigated.

Table 1

Experiments: locations and years
Doświadczenia: miejscowości i lata

Trial Doświadczenie	Location / experimental stadion Miejscowość/ stacja doświadczalna	Year Rok
1	Évora	2002, 2004
2	Herdade da Comenda	2003, 2004
3	E.N.M.P.	2002, 2003, 2004
4	Beja	2002, 2004
5	Benavila	2002
6	Portalegre	2003

Table 2

Experiments: genotypes names
Doświadczenia: nazwy genotypów

S. MATEUS	AE9402	87SA29	AVON*S.MATEUS
St. ALEIXO	AE9403	COBER79-19	COBER79-19*AVON
AE9301	AE9701	S.VICENTE*COBER	X2795/IJUIL1743
AE9302	AE9702	S.VICENTE*AE8303	TX88AB1494
AE9303	AE9703	QR772	
AE9401	Sta. EULÁLIA	QR720	

3.1. Year by year analysis

3.1.1 Regression adjustments

In Table 3 we present the adjusted coefficients and the corresponding R^2 for the years 2002, 2003 and 2004. The results were obtained using Zig-Zag algorithm, after 4 interations.

Adjusted coefficients and *R²*: years 2002, 2003 and 2004
Poprawione współczynniki regresji i *R²*: Lata: 2002, 2003 i 2004

Year Rok Genotype Genotyp	2002			2003			2004		
	$\tilde{\alpha}$	$\tilde{\beta}$	R²	$\tilde{\alpha}$	$\tilde{\beta}$	R²	$\tilde{\alpha}$	$\tilde{\beta}$	R²
S.VICENTE*AE8303	-1141.5	1.411	0.985	421.65	0.620	0.356	-305.69	1.064	0.856
COBER79-19	-908.54	1.359	0.852	-115.41	1.202	0.694	-269.78	1.101	0.874
AE9403	-800.02	1.30	0.947	1020.59	0.347	0.321	69.26	1.036	0.949
AE9302	-646.85	1.292	0.952	162.79	0.802	0.633	-340.35	1.064	0.917
AE9301	-1040.67	1.277	0.953	114.02	0.731	0.755	-335.22	1.033	0.893
AE9401	-370.62	1.172	0.972	234.64	0.843	0.441	560.14	0.881	0.873
S.MATEUS	-408.15	1.144	0.904	-376.41	1.218	0.847	-719.53	0.980	0.867
TX88AB1494	-264.67	1.059	0.857	462.81	0.730	0.752	1069.64	0.734	0.785
AE9303	332.33	1.042	0.867	-322.89	1.685	0.961	729.17	0.926	0.899
S. VICENTE*COBER	173.75	1.01	0.784	55.86	0.793	0.387	555.73	0.923	0.832
AE9703	11.72	1.004	0.876	-229.74	0.771	0.432	-317.56	1.186	0.942
AE9402	-213.97	0.994	0.918	388.9	0.626	0.601	879.02	0.724	0.844
X2795/IJUIL1743	87.23	0.984	0.798	-362.43	1.383	0.760	-426.55	1.102	0.851
AVON*S.MATEUS	572.03	0.903	0.945	278.52	0.844	0.670	681.80	0.925	0.866
AE9702	-117.22	0.866	0.908	421.8	0.783	0.705	-142.46	1.079	0.915
AE9701	98.79	0.837	0.820	983.05	0.347	0.759	992.15	0.709	0.848
COBER79-19*AVON	207.55	0.834	0.938	115.31	0.530	0.761	299.46	0.820	0.850
Sta EULÁLIA	495.67	0.823	0.708	-3.34	1.125	0.490	-189.29	0.982	0.826
87SA29	2091.39	0.692	0.493	-869.55	1.952	0.801	-994.76	1.390	0.916
QR720	1305.55	0.602	0.525	-607.92	1.491	0.697	-41.33	0.985	0.899
ST. ALEIXO	998.58	0.598	0.723	-383.78	1.146	0.935	-505.99	1.114	0.759
QR772	1145.6	0.566	0.649	-639.43	1.514	0.823	-580.82	1.072	0.933

The ranges of environmental indexes were as follows:

For year 2002— [2444.77 ; 5225.95];

For year 2003 — [701.45 ; 1945.91];

For year 2004 — [1823.73 ; 4915.15].

3.1.2 Upper contour analysis

According to Mexia *et al* (1997), the representation of all the adjusted regression lines defines a convex polygonal as the upper contour. The genotypes whose adjusted regressions partake of the upper contour are dominant, and each dominant genotype has a dominance range. Non dominant genotypes should be compared with the dominant ones to test if they are significantly dominated, or not. In Figures 1, 2 and 3 we present the graphics for the adjusted linear regressions to the years 2002, 2003 and 2004, respectively.

In 2002, considering the entire dominance range of environmental indexes [2444.77 ; 225.95]; we observe two dominant genotypes: 87SA29 dominant in [2447.77 ; 4496.37] and S.VICENTE*AE8303 dominant in [4496.37 ; 5225.95]. To see which genotypes are dominated by 87SA29 in the leftmost range and by S.VICENTE*AE8303 in the rightmost range, we made the following multiple comparisons:

— at point 2444.77 we had to compare 87SA29 with the genotypes with lesser adjusted slopes;
— at point 4496.37 we had to compare 87SA29 with the genotypes with larger adjusted slopes;
— at point 4496.37 we had to compare S.VICENTE*AE8303 with all the other genotypes.
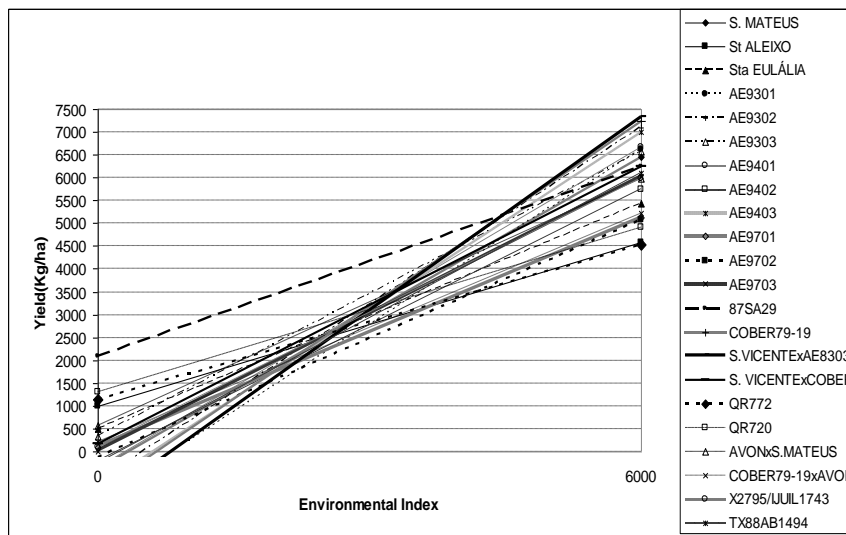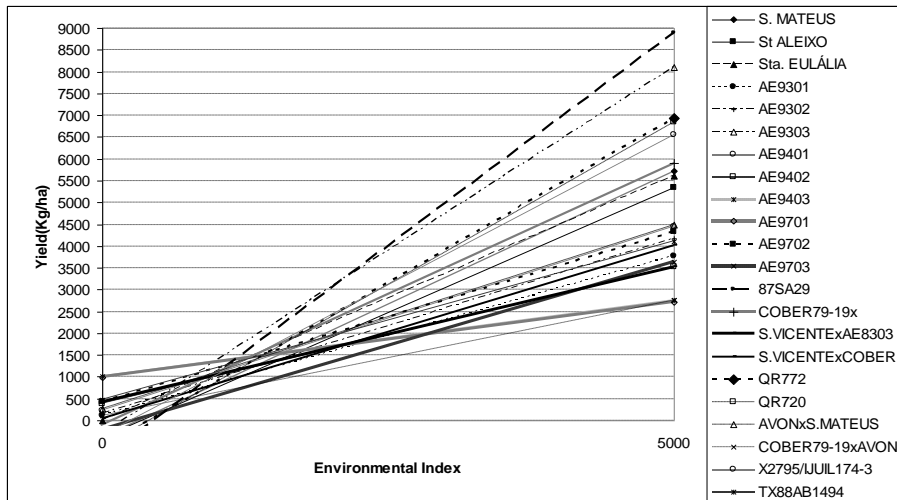

Fig. 1. Upper contour for oat genotypes in 2002
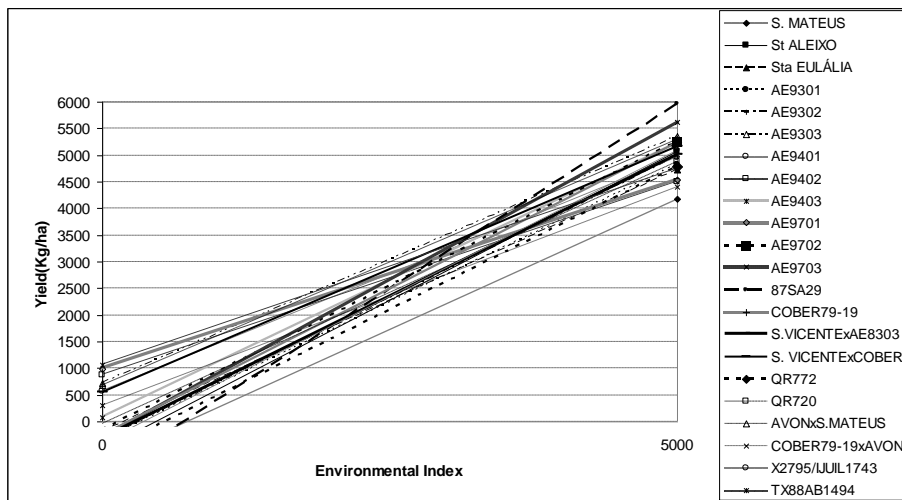**Rys. 1. Górny kontur dla genotypów owsa w 2002**

In 2003, considering the entire dominance range of environmental indexes [701.45 ; 1945.91], we observe two dominant genotypes: AE9403 dominant in [701.45 ; 1004.1] and AE9303 dominant in [1004.1 ; 1945.91].

To see which genotypes are dominated by AE9403 in the leftmost range and by AE9303 in the rightmost range, the following multiple comparisons were made:
— at point 701.45 we had to compare AE9403 with the genotypes with lesser adjusted slopes;
— at point 1004.1 we had to compare AE9403 with the genotypes with larger adjusted slopes;
— at point 1004.1 we had to compare AE9303 with the genotypes with lesser adjusted slopes;
— at point 1945.91 we had to compare AE9303 with the genotypes with larger adjusted slopes;

Fig. 2. Upper contour for oat genotypes in 2003
Rys. 2. Górny kontur dla genotypów owsa w 2003

Fig. 3. Upper contour for oat genotypes in 2004
Rys. 3. Górny kontur dla genotypów owsa w 2004

In 2004, considering the entire dominance range of environmental indexes [1823.73 ; 4915.15], we observe two dominant genotypes: AE9303 dominant in [1823.73 ; 3715.37] and 87SA29 dominant in [3715.37 ; 4915.15].

To see which genotypes are dominated by AE9303 in the leftmost range and by 87SA29 in the rightmost range, we made out the following multiple comparisons:

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— at point 1823.73 we had to compare AE9303 with the genotypes with lesser adjusted slopes;

— at point 3715.37 we had to compare AE9303 with the genotypes with larger adjusted slopes;

— at point 3715.37 we had to compare 87SA29 with the genotypes with lesser adjusted slopes;

3.1.3 Multiple comparison tests

Tables 4, 5 and 6 show the results on genotypes comparison in the years 2002, 2003 and 2004, respectively using Scheffé, Tukey and Bonferroni methods at the 5% level of significance.

Table 4

Significantly dominated genotypes in 2002
Istotnie dominujące genotypy w roku 2002

Method Metoda	87SA29 $x_0 = 2444.77$	87SA29 $x_0 = 4496.37$	S.VICENTE*AE8303 $x_0 = 4496.37$
Scheffé	QR720, ST ALEIXO, QR772	AE9702, AE9701, COBER79-19*AVON	AE9702, AE9701, COBER79-19*AVON, QR720, ST ALEIXO, QR772
Bonferroni	QR720, ST ALEIXO, QR772	TX88AB1494, AE9402, AE9702, AE9701, COBER79-19*AVON, STA EULÁLIA	AE9301, S. MATEUS, TX88AB1494, S.VICENTE*COBER, AE9703, AE9402, X2795/IJUIL1743, AVON*S.MATEUS, AE9702, AE9701, COBER79-19*AVON, STA EULÁLIA, QR720, ST ALEIXO, QR772
Tukey	QR720, ST ALEIXO, QR772	AE9301, S. MATEUS, TX88AB1494, S. VICENTE*COBER, AE9703, AE9402, X2795/IJUIL1743, AVON*S.MATEUS, AE9702, AE9701, COBER79-19*AVON, STA EULÁLIA	TX88AB1494, AE9402, AE9702, AE9701, COBER79-19*AVON, STA EULÁLIA, QR720, ST ALEIXO, QR772

Table 5

Significantly dominated genotypes in 2003
Istotnie dominujące genotypy w roku 2003

Method Metoda	AE9403 $x_0 = 701.45$	AE9403 $x_0 = 1004.1$	AE9303 $x_0 = 1004.1$	AE9303 $x_0 = 1945.91$
Scheffé	---	---	---	---
Bonferroni	---	S. MATEUS, ST. ALEIXO, S.VICENTExCOBER, AE9703, AE9301, COBER79-19xAVON	QR772, QR720, S. MATEUS, ST. ALEIXO, S.VICENTExCOBER, AE9703, AE9301, COBER79-19xAVON, AE9701	---
Tukey	---	---	---	---

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Table 6

Significantly dominated genotypes in 2004
Istotnie dominujące genotypy w roku 2004

Method Metoda	AE9303 $x_0 = 1823.73$	AE9303 $x_0 = 3715.37$	87SA29 $x_0 = 3715.37$
Scheffé	---	---	---
Bonferroni	AE9702, AE9703, COBER79-19xAVON	---	QR772, QR720, COBER79-19, ST ALEIXO, STA EULÁLIA, AE9401, AE9302, S. VICENTE x COBER, AE9702, S.VICENTExAE8303, AE9403, AE9701
Tukey	---	---	AE9702

3.2 Over years analysis

3.2.1 Regression adjustments

Table 7 contains the adjusted coefficients and the corresponding R^2. These results were obtained using the Zig-Zag algorithm, after 4 iterations. The genotypes are presented according to decreasing adjusted slopes order.

Table 7

Adjusted coefficients and R^2
Poprawione współczynniki regresji oraz R^2

Genotype — Genotyp	$\tilde{\alpha}$	$\tilde{\beta}$	R^2
AE9703	-564.36	1.19	0.911
S.VICENTE*AE8303	-457.06	1.178	0.914
AE9302	-407.0	1.168	0.934
87SA29	140.16	1.164	0.775
COBER79-19	-213.72	1.146	0.871
AE9301	-469.20	1.103	0.937
AE9403	-72.43	1.09	0.929
S. VICENTE*COBER	-73.83	1.079	0.853
AE9401	39.98	1.046	0.913
S. MATEUS	-345.86	1.031	0.845
X2795/IJUIL1743	17.53	1.003	0.851
AVON*S.MATEUS	274.11	1.002	0.918
AE9303	611.61	0.978	0.899
COBER79-19*AVON	-191.61	0.938	0.911
TX88AB1494	345.51	0.913	0.860
St. ALEIXO	9.95	0.909	0.802
AE9402	182.15	0.898	0.894
Sta EULÁLIA	230.58	0.888	0.791
QR720	298.62	0.885	0.797
AE9702	227.41	0.862	0.85
QR772	214.82	0.839	0.819
AE9701	539.32	0.763	0.83

In our problem the range of environmental indexes was [701.45 ; 5225.95].

3.2.2 Upper contour analysis

Figure 4 shows a graphic for the adjusted linear regressions over the years 2002, 2003 and 2004.

Considering the entire dominance range of environmental indexes over years, [701.45 ; 5225.95], we find two dominant genotypes: AE9303 dominant in [701.45 ; 2534.68] and 87SA29 dominant in [2534.68 ; 5225.95].
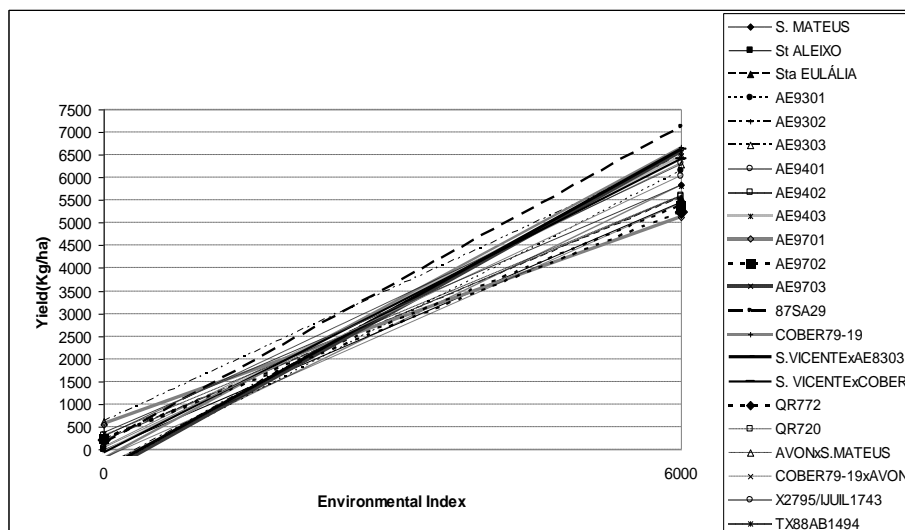

Fig. 4. Upper contour for oat genotypes
Rys. 4. Górny kontur dla genotypów owsa

Table 8

Significantly dominated genotypes
Istotnie dominujące genotypy

Method Metoda	AE9303 $x_0 = 701.45$	AE9303 $x_0 = 2534.68$	87SA29 $x_0 = 2534.68$
Scheffé	---	AE9301, S. MATEUS	AE9301, S. MATEUS, X2795/IJUIL1743, COBER79-19*AVON, TX88AB1494, St. ALEIXO, AE9402, Sta EULÁLIA, QR720, AE9702, QR772, AE9701
Bonferroni	COBER79-19*AVON, St. ALEIXO, AE9402, AE9702, QR772	AE9703, S.VICENTE*AE8303, AE9302, COBER79-19, AE9301, AE9403, S. VICENTE*COBER, AE9401, S. MATEUS, X2795/IJUIL1743, AVON*S.MATEUS, COBER79-19*AVON, TX88AB1494, St. ALEIXO, AE9402, Sta EULÁLIA, QR720, AE9702, QR772, AE9701	AE9703, S.VICENTE*AE8303, AE9302, COBER79-19, AE9301, AE9403, S. VICENTE*COBER, AE9401, S. MATEUS, X2795/IJUIL1743, AVON*S.MATEUS, AE9303, COBER79-19*AVON, TX88AB1494, St. ALEIXO, AE9402, Sta EULÁLIA, QR720, AE9702, QR772, AE9701
Tukey	---	AE9703, S.VICENTExAE8303, AE9302, AE9301, S.MATEUS, X2795/IJUIL1743	AE9301, S. MATEUS, X2795/IJUIL1743, COBER79-19*AVON, TX88AB1494, St. ALEIXO, AE9402, Sta EULÁLIA, QR720, AE9702, QR772, AE9701

To see which genotypes are dominated by AE9303 in the leftmost range and by 87SA29 in the rightmost range, we made the following multiple comparisons:

— at point 701.45 we had to compare AE9303 with the genotypes with lesser adjusted slopes;
— at point 2534.68 we had to compare AE9303 with the genotypes with larger adjusted slopes;
— at point 2534.68 we had to compare 87SA29 with the genotypes with lesser adjusted slopes;

3.2.3 Multiple comparison tests

Table 8 contains the results on genotype comparison using Scheffé, Tukey and Bonferroni methods, at the 5% level of significance.

3.3 Synthesis on multiple comparisons

A global analysis on multiple comparisons year by year and over years is presented in Table 9.

Table 9

Global analysis on the multiple comparisons
Synteza na podstawie testów wielokrotnych

Genotypes —Genotypy	Year by year						Over years
	2002	2003	2004	NyD	Nyd		2002/2003/2004
AE9703	d	d	d	0	3		d
S.VICENTE*AE8303	R		d	1	1		d
AE9302			d	0	1		d
87SA29	L		R	2	0		R
COBER79-19			d	0	1		d
AE9301	d	d		0	2		d
AE9403		L	d	1	1		d
S. VICENTE*COBER	d	d	d	0	3		d
AE9401			d	0	1		d
S. MATEUS	d	d		0	2		d
X2795/IJUIL1743	d			0	1		d
AVON*S.MATEUS	d			0	1		d
AE9303		R	L	2	0		L
COBER79-19*AVON	d	d	d	0	3		d
TX88AB1494	d			0	1		d
St. ALEIXO	d	d	d	0	3		d
AE9402	d			0	1		d
Sta EULÁLIA	d		d	0	2		d
QR720	d		d	0	3		d
AE9702	d		d	0	2		d
QR772	d	d	d	0	3		d
AE9701	d	d	d	0	3		d
Number of dominant genotypes at the 5% level of significance	2	2	2				2
Number of dominated genotypes at the 5% level of significance	15	8	14				20

NyD — number of years in which the genotype was dominant
Nyd — number of years in which the genotype was dominated
d — significantly dominated genotype, at 5% level of significance
R — dominant genotype at the rightmost range
L — dominant genotype at the leftmost range

The data show that considering both kinds of analysis, year by year and over years, we always have two dominant genotypes at the 5% level of significance. In 2002 we have 15 dominated genotypes, in 2003 — 8 dominated genotypes, and in 2004 — 14 dominated genotypes, while the over years analysis resulted in 20 dominated genotypes, at the 5% level of significance.

4. CONCLUSION

According to the JRA year by year, in the year 2002 the genotypes S.VICENTE*AE8303 and 87SA29 could be recommended as the preferable ones in program evaluation; in 2003 the best genotypes were AE9403 and AE9303; in 2004 we should select 87SA29 and AE9303. In the over years analysis we can see that 87SA29 and AE9303 are the recommendable genotypes.

It can be concluded that it is not a good way to select genotypes based on the year by year analysis alone. It is seen that, for example in 2002, the genotype 87SA29 was dominant at the leftmost range, whereas in 2003 it was neither dominant nor dominated, not too relevant. However, in 2004, this genotype could be again dominant, and according to the over years on analysis it is one of the best two genotypes.

Genotype AE9303 was neither dominant nor dominated in 2002, and it was dominant in 2003 and 2004 and can be recommended in the over years analysis.

It is also to be pointed out that the over years analysis is likely to be very discriminate in what concerns significantly dominated genotypes, but very important in selection of dominant genotypes. The results of the over year analysis show that only two types of genotypes have been identified: dominant genotypes and dominated genotypes.

In a plant breeding program we should take into account the results of both analyses to draw proper conclusions. The year by year analysis is important, but when taken alone, it may cause the risk of discarding good genotypes. Comparatively, over years analysis is very important in selecting the most promising genotypes, but in the case of our studies it was not flexible enough to distinguish intermediate oat genotypes.

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